

0702

7



OIEP

RAW SEQUENCE LISTING

DATE: 07/12/2002

PATENT APPLICATION: US/09/883,343A

TIME: 09:54:49

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Output Set: N:\CRF3\07122002\I883343A.raw

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1 <110> APPLICANT: Stiles, Michael E.
2   Vederas, John C.
3   van Belkum, Marius J.
4   Worobo, Randy W.
5   Worobo, Rodney J.
6   Greer, G. Gordon
7   McMullen, Lynn M.
8   Leisner, Jorgen J.
9   Poon, Alston
10  Franz, Charles M.A.P.
11 <120> TITLE OF INVENTION: NovelBacteriocins, Transport and Vector System and Method of
Use
12 <130> FILE REFERENCE: 660.0005US
13 <140> CURRENT APPLICATION NUMBER: 09/883,343A
C--> 14 <141> CURRENT FILING DATE: 2001-06-19
17 <150> PRIOR APPLICATION NUMBER: US/08/924,629
18 <151> PRIOR FILING DATE: 1997-09-05
21 <150> PRIOR APPLICATION NUMBER: US 60/026,257
22 <151> PRIOR FILING DATE: 1996-09-05
23 <160> NUMBER OF SEQ ID NOS: 80
24 <170> SOFTWARE: PatentIn version 3.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 184
28 <212> TYPE: DNA
29 <213> ORGANISM: Divergicin A
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32 <222> LOCATION: (24)..(28)
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34 <221> NAME/KEY: CDS
35 <222> LOCATION: (38)..(184)
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39 <223> OTHER INFORMATION:
W--> 40 <221> primer_bind
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48   Met Lys Lys Gln Ile Leu

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49                                     1                               5
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51   Lys Gly Leu Val Ile Val Val Cys Leu Ser Gly Ala Thr Phe Phe Ser
52                                     10                               15                               20
53   aca cca caa caa gct tct gct gta aat tat ggt aat ggt gtt tct tgc      151
54   Thr Pro Gln Gln Ala Ser Ala Val Asn Tyr Gly Asn Gly Val Ser Cys
55                                     25                               30                               35
56   agt aaa aca aaa tgt tca gtt aac tgg gga caa                        184
57   Ser Lys Thr Lys Cys Ser Val Asn Trp Gly Gln
58   40                               45

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97   caagagttaa atatttctca actgccttct ttaattttta ctaatggaaa catggactat      180
98   aaacgattat caatttatac aattaaaaca ccaataaatg catggattac tgctattaat      240
99   gacgaattaa ttccaaaaca ttccaagcaa tcatcaacaa attaaaaatg gttaagggtca      300
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103	cgctagactt	tgaaccatg	ccgatccagg	ctgatttgag	tttattcgat	aaaaaggatt	540
104	taccctatcc	ttttatcgcc	catgtcatta	aagacggtaa	ataccgcgat	tattatgtag	600
105	tttatgggat	caaaggtgat	cagctattaa	tcgctgatcc	agataatacc	gttggtaaaa	660
106	ataaaatgac	aaaagcgc	tttaatgagg	agtggaccgg	tgtgtccatt	tttattgcgc	720
107	ccaatccaac	ctacaagcca	acaaaggata	aaaagcgttc	cttgacttct	tttattccag	780
108	tgattacgcg	tcaaaaatta	ttagttatca	atattgtcat	tgtgccttgg	ttggttacc	840
109	tagtgagtat	tttaggatca	tattatttgc	aaggatcat	tgatacctat	atccccgata	900
110	acatgaaaaa	caccctaggg	attgtgtcac	tagggcttat	ttttgcgtat	gttatccaac	960
111	aactgctctc	ttatgccaga	gattatttat	taattgtcat	ggggcaacgc	ctctcaattg	1020
112	atattatttt	gtcttatatc	aaacacattt	ttgaactgcc	aatgtctttt	ttcgcgacgc	1080
113	gtcgtaccgg	tgaattgtg	agccgtttta	cggacgctaa	tgccattatt	gaagccctgg	1140
114	caagcacgat	gttatctgta	tttttagact	taggaatttt	ggtcattgtt	ggcacagtgc	1200
115	tagtggttca	aaattcaacc	ttgtttctga	tttctctgat	tgccattccg	gcttatgccc	1260
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117	gttcgatgtt	aagttcttcc	attattgaag	atattaatgg	cgttgagacg	attaaagcgc	1380
118	tgaatagtga	agaaaccgcc	tatcataaaa	ttgatcatga	atttgtcact	tatttagaaa	1440
119	aatcatttgt	ttacgctaaa	acagaagcca	ctcaaaatgc	gattaaaagc	ctcttacagc	1500
120	tctctttaaa	tgtcgtgatc	ttatgggttg	gcgcacaact	ggtcatgacc	aataaaatta	1560
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122	atattattaa	tttacaact	aagctccaac	aggcctcagt	cgctaataat	cgtttgaacg	1680
123	aagtttattt	ggttgattca	gaatttaaag	ctagtcatca	aatgacagaa	agcattatgc	1740
124	ccaatagctc	attagtagcc	gatcatatca	cctataaata	cggttttggg	gcgccagcaa	1800
125	ttgatgatgt	ttcactaacg	attacagccg	gtgaaaaaat	cgttttgggt	gggattagt	1860
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127	caatttcaat	aggacaaaca	ccactcgcca	atcttgataa	acatgagcta	agagcacaca	1980
128	ttaattattt	accacaagaa	ccctttatat	tttccggttc	aattatggac	aacctgttat	2040
129	tgggggctaa	gccagggaca	acccaagaag	atattatcag	ggcggtagaa	attgctgaaa	2100
130	ttaaagatga	tattgaaaaa	atgtcgcaag	gatttggcac	tgaactcgca	gaaagtggca	2160
131	atatttcggg	tggtcaaaaa	caacgcattg	cttttagctag	agccatttta	gtcgattctc	2220
132	cgggtgctgat	tttagatgag	tcaaccagta	atcttgatgt	tttaacagaa	aaaaagatta	2280
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136	acctgatgtt	tgatccaaaa	tacttagaaa	gtggcgaatt	ttatcaacgt	cgttaccgca	2520
137	attttccaac	tctgattatt	gtgcctat	ttttgttagt	cgtgtttatc	attctattta	2580
138	gcctatttgc	taagcgtgaa	attgttgtca	aagcaagtgg	cgaaattatt	ccagccaaa	2640
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141	cgtctcaatt	actgacgcaa	caacttaata	atcttaacga	cgtctaaaa	agtcttgata	2820
142	cctataagca	gagtattgtt	aacggacgta	gcgaatttgg	tgccacagat	caatttgggt	2880
143	atgatagtct	attcaacggc	tatatggcgc	aagttgatac	gttgacgagt	gaatttaatc	2940
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145	aacaaggtca	atctaaaaac	aatcaacaat	tagctaatta	tcaagctatt	ctaaccagta	3060
146	ttaaatagcaa	cactaaaccg	actaataatc	cctatcaagc	catttatgat	aattattcag	3120
147	cccagttaaa	atcagcacia	acaactgatg	ataaagatca	agtcaagcaa	attgccttaa	3180
148	gtaatgtaca	acaacaaatt	gatcaattac	aaacaacgag	tagttcgtat	gatagtcaaa	3240
149	ttgctgggtat	tacaaagagt	ggtcctttat	ctcaaagcag	taccttagat	aaaatcgctg	3300

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152 aagcaccaga agatggcatt ttacatttag ccactgacaa aactaaaatc aagtatttcc 3480
153 ctaaaggcac aaccattgcg caaatattatc ctaaactgac gcaaaaaaca gctttgaatg 3540
154 ttgagtacta tgtgcctgcc agtaatatta tcggcttaaa gcaaagacaa gccatccggt 3600
155 ttgtagcaaa tcaaaatgtc acgaaaccgc tcaccttaaa cgggaacaatc aaaagcatta 3660
156 gttctgcaac aatagccagt aaagagggat ccttttataa attagtcgcy acgattcagg 3720
157 ctagcaaaa agaccgtgaa cagattaaat atggctcttaa tggctcgaatc acaaccataa 3780
158 aagggaactaa aacatgggtt aattattata aagacattgt tttaggtgag aataattagc 3840
159 taggaagata aacacaattt ttaaacgtgt ttatctttt tagtctcaat gaaattgtcg 3900
160 ccgaagggtt ttctagccaa gtggcaggac acagaaaaat gatagttgct actgaaggga 3960
161 agttcaactg ccaccaaaaa tagtaaccgc gcgacagcca accgccacca caacagttat 4020
162 gctcgcccggt gggtattatt atcatthaaca ctcttacgtc tttctatgat acttttgagc 4080
163 cacattctta taatgctgca atcgaccttt tagaaaattg atctcatcag aaatttcttt 4140
164 taagtgggta tcatcagcat gtttactagc aatatttaaat tctttaatcc tacgtttaat 4200
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169 <211> LENGTH: 717

170 <212> TYPE: PRT

171 <213> ORGANISM: lcaC;

172 <400> SEQUENCE: 5

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178 35 40 45
179 Thr Thr Ala Leu Gly Ile Val Lys Ala Ala Asn Ala Leu Asp Phe Glu
180 50 55 60
181 Thr Met Pro Ile Gln Ala Asp Leu Ser Leu Phe Asp Lys Lys Asp Leu
182 65 70 75 80
183 Pro Tyr Pro Phe Ile Ala His Val Ile Lys Asp Gly Lys Tyr Pro His
184 85 90 95
185 Tyr Tyr Val Val Tyr Gly Ile Lys Gly Asp Gln Leu Leu Ile Ala Asp
186 100 105 110
187 Pro Asp Asn Thr Val Gly Lys Asn Lys Met Thr Lys Ala His Phe Asn
188 115 120 125
189 Glu Glu Trp Thr Gly Val Ser Ile Phe Ile Ala Pro Asn Pro Thr Tyr
190 130 135 140
191 Lys Pro Thr Lys Asp Lys Lys Arg Ser Leu Thr Ser Phe Ile Pro Val
192 145 150 155 160
193 Ile Thr Arg Gln Lys Leu Leu Val Ile Asn Ile Val Ile Ala Ala Leu
194 165 170 175
195 Leu Val Thr Leu Val Ser Ile Leu Gly Ser Tyr Tyr Leu Gln Gly Ile
196 180 185 190
197 Ile Asp Thr Tyr Ile Pro Asp Asn Met Lys Asn Thr Leu Gly Ile Val
198 195 200 205
199 Ser Leu Gly Leu Ile Phe Ala Tyr Val Ile Gln Gln Leu Leu Ser Tyr

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201	Ala Arg Asp Tyr Leu	Leu Ile Val Met Gly Gln Arg Leu Ser Ile Asp	
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203	Ile Ile Leu Ser Tyr	Ile Lys His Ile Phe Glu Leu Pro Met Ser Phe	240
204	245	250	255
205	Phe Ala Thr Arg Arg Thr Gly Glu Ile Val Ser Arg Phe Thr Asp Ala		
206	260	265	270
207	Asn Ala Ile Ile Glu Ala Leu Ala Ser Thr Met Leu Ser Val Phe Leu		
208	275	280	285
209	Asp Leu Gly Ile Leu Val Ile Val Gly Thr Val Leu Val Val Gln Asn		
210	290	295	300
211	Ser Thr Leu Phe Leu Ile Ser Leu Ile Ala Ile Pro Ala Tyr Ala Leu		
212	305	310	315
213	Val Val Trp Leu Phe Met Arg Pro Phe Ser Lys Met Asn Asn Asp Gln		
214	325	330	335
215	Met Gln Ala Gly Ser Met Leu Ser Ser Ser Ile Ile Glu Asp Ile Asn		
216	340	345	350
217	Gly Val Glu Thr Ile Lys Ala Leu Asn Ser Glu Glu Thr Ala Tyr His		
218	355	360	365
219	Lys Ile Asp His Glu Phe Val Thr Tyr Leu Glu Lys Ser Phe Val Tyr		
220	370	375	380
221	Ala Lys Thr Glu Ala Thr Gln Asn Ala Ile Lys Ser Leu Leu Gln Leu		
222	385	390	395
223	Ser Leu Asn Val Val Ile Leu Trp Val Gly Ala Gln Leu Val Met Thr		
224	405	410	415
225	Asn Lys Ile Ser Val Gly Gln Leu Ile Thr Tyr Asn Ala Leu Leu Gly		
226	420	425	430
227	Phe Phe Thr Asp Pro Leu Gln Asn Ile Ile Asn Leu Gln Thr Lys Leu		
228	435	440	445
229	Gln Gln Ala Ser Val Ala Asn Asn Arg Leu Asn Glu Val Tyr Leu Val		
230	450	455	460
231	Asp Ser Glu Phe Lys Ala Ser His Gln Met Thr Glu Ser Ile Met Pro		
232	465	470	475
233	Asn Ser Ser Leu Val Ala Asp His Ile Thr Tyr Lys Tyr Gly Phe Gly		
234	485	490	495
235	Ala Pro Ala Ile Asp Asp Val Ser Leu Thr Ile Thr Ala Gly Glu Lys		
236	500	505	510
237	Ile Ala Leu Val Gly Ile Ser Gly Ser Gly Lys Ser Thr Leu Val Lys		
238	515	520	525
239	Leu Leu Val Asn Phe Phe Gln Pro Glu Ser Gly Thr Ile Ser Leu Gly		
240	530	535	540
241	Gln Thr Pro Leu Ala Asn Leu Asp Lys His Glu Leu Arg Ala His Ile		
242	545	550	555
243	Asn Tyr Leu Pro Gln Glu Pro Phe Ile Phe Ser Gly Ser Ile Met Asp		
244	565	570	575
245	Asn Leu Leu Leu Gly Ala Lys Pro Gly Thr Thr Gln Glu Asp Ile Ile		
246	580	585	590
247	Arg Ala Val Glu Ile Ala Glu Ile Lys Asp Asp Ile Glu Lys Met Ser		
248	595	600	605

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:67; Xaa Pos. 13,15,21,30
Seq#:70; Xaa Pos. 33,37,40,41
Seq#:75; Xaa Pos. 25,26,28,29,31

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 11

VERIFICATION SUMMARY

DATE: 07/12/2002

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L:37 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:40 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:43 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:333 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:359 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:383 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:407 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:606 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:22
L:670 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:730 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29
L:877 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:36
L:934 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
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L:1433 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:67
L:1434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:0
L:1436 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:16
L:1476 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:70
L:1479 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:70
L:1482 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:70
L:1487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:32
L:1559 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:75
L:1562 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:75
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L:1568 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:75
L:1571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:16